

```

RESULT 1
CTE245577/c
LOCUS
DEFINITION
CTE245577
Cymopsis tetragonoloba partial 5.8S rRNA gene and ITS 2, isolate
seed 10.
405 bp
DNA
linear
PLN 06-AUG-2002
ACCESSION
AJ245577
1
GI:22138754
268 ribosomal RNA; 26S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA
gene; internal transcribed spacer 2; ITS2.
VERSION
AJ245577
1
GI:22138754
268 ribosomal RNA; 26S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA
gene; internal transcribed spacer 2; ITS2.
KEYWORDS
Cymopsis tetragonoloba (guar)
Cymopsis tetragonoloba
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Indigoferaceae; Cymopsis.
SOURCE
1
Domenech-Sanchez,A., Hernandez,M.L., Rosello,J.A. and Benedi,V.J.
Method for detecting additions of guar gum to locust bean gum
Unpublished
2
(bases 1 to 405)
Domenech-Sanchez,A.
Direct Submission
TITLE
Submitted (05-AUG-1999) Domenech-Sanchez A., Biologia, Area de
Microbiologia, Universitat de les Illes Balears and IMEDA
(CSIC-UIB), Carrtera de Valldemossa, km 7,5; Palma de Mallorca,
07071, SPAIN
FEATURES
Location/Qualifiers
1..405
/organism="Cymopsis tetragonoloba"
/mol_type="genomic DNA"
/isolate="seed 10"
/db_xref="taxon:3832"
/tissue_type="seed"
/country="India"
1..129
/gene="5.8S rRNA"
<1..129
/gene="5.8S rRNA"
/product="5.8S ribosomal RNA"
130..346
/misc_feature
/note="internal transcribed spacer 2, ITS2"
347..405
/gene

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2005, 05:41:19 ; Search time 220.513 Seconds
(without alignments)
536.907 Million cell updates/sec

Title: US-10-009-980B-5
Perfect score: 20
Sequence: 1 tccaaacaagatggagctg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001as:*
5: Geneseq2001bs:*
6: Geneseq2002as:*
7: Geneseq2002bs:*
8: Geneseq2003as:*
9: Geneseq2003bs:*
10: Geneseq2003cs:*
11: Geneseq2003ds:*
12: Geneseq2004as:*
13: Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	4	AAH44594
2	20	100.0	405	4	AAH44598
3	17	85.0	278	6	ABL85231
4	16.8	84.0	1452	4	AAH45172
5	16.8	84.0	110000	6	ABQ69245_16
6	16.8	84.0	110000	6	ABQ67195_10
7	16.4	82.0	187	12	ADJ67333
8	16.4	82.0	599	12	ADM72157
9	16.4	82.0	1431	3	AAA38955
10	16.4	82.0	15456	4	AAC85008
11	16.4	82.0	15456	6	AAC85009
12	16.4	82.0	15456	6	AAD27765
13	16.4	82.0	15456	6	AAD27766
14	16.4	82.0	52479	9	ADA02795
15	16.4	82.0	52479	10	ADB72533
16	16.4	82.0	52479	10	ADC85275
17	16.4	82.0	52479	12	ADM74390
18	16	80.0	540	3	AAA81688
19	16	80.0	49088	11	ACN43856
20	15.8	79.0	269	6	ABL87432

21	15.8	79.0	280	12	ADI42908
22	15.8	79.0	280	12	ADO03087
C	23	15.8	392	5	AAS64572
C	24	15.8	400	2	AAV78107
C	25	15.8	401	4	AAK95811
C	26	15.8	401	4	AAK97304
C	27	15.8	401	6	ABT00581
C	28	15.8	401	6	ABT02074
C	29	15.8	431	3	AAC10517
C	30	15.8	457	9	ACH47452
C	31	15.8	503	6	ABL78849
C	32	15.8	553	4	AAI17661
C	33	15.8	553	4	ABA62599
C	34	15.8	553	4	AAI42592
C	35	15.8	553	4	ABA29922
C	36	15.8	553	4	AAK36807
C	37	15.8	553	4	AAK36807
C	38	15.8	553	4	AAK36807
C	39	15.8	553	4	ABT00581
C	40	15.8	553	6	ABT02074
41	15.8	79.0	561	4	AAI20007
42	15.8	79.0	561	4	ABA65035
43	15.8	79.0	561	4	AAI45205
44	15.8	79.0	561	4	ABA47151
45	15.8	79.0	561	4	AAK39197

ALIGNMENTS

RESULT 1
AAH44594
ID AAH44594 standard; DNA; 20 BP.

AC AAH44594;

DT 01-NOV-2001 (first entry)

Guar and locust bean seed differentiation PCR primer PG21.

Guar gum; locust bean gum; detection; plant; initiator; amplification;
PCR; Cyamopsis tetragonoloba; Ceratonia siliqua; thickener;
gelling agent; food stabiliser; differentiation; PCR primer; ss.

OS Synthetic.

PN WO200166794-A1.

PD 13-SEP-2001.

PF 02-MAR-2001; 2001WO-ES000079.

PR 08-MAR-2000; 2000ES-00000560.

(CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.

(UYIS-) UNIV LAS ISLAS BALEARES.

(UYVA-) UNIV VALENCIA.

(CARO-) CAROB SA.

PI Benedi Benito VJ, Domenech Sanchez A, Hernandez Viadel Ml;

PI Alberti Serrano S, Rossello Picornell JA;

DR WPI; 2001-565598/63.

XX Differentiating between guar and locust bean seeds, or derived gums, by
amplifying specific, characteristic regions of ribosomal DNA.

PS Claim 4; Fig 1; 44pp; Spanish.

CC The present invention describes a method for differentiating between
seeds of Cyamopsis tetragonoloba (guar) and Ceratonia siliqua (locust
bean) from differences in rDNA extracted from them. The seeds are
germinated, DNA extracted and amplified by polymerase chain reaction

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2005, 06:13:55 ; Search time 1760 Seconds
(without alignments)
432.549 Million cell updates/sec

Title: US-10-009-980B-5

Perfect score: 20

Sequence: 1 tccaacaagaagtgagtcg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 69479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gse1:*

9: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	18.4	92.0	941	AZ541838	AZ541838 ENTFO93TR
2	18	90.0	374	AJ012952	AJ012952 EBEST102
3	18	90.0	464	CN199108	CN199108 TGETZy15
4	18	90.0	527	AF348499	AF348499 AF348499
5	18	90.0	864	AZ679167	AZ679167 ENTJP67TR
6	18	90.0	873	BH152072	BH152072 ENTJP94TF
7	18	90.0	888	AZ683940	AZ683940 ENTHX10TR
8	18	90.0	962	BH151479	BH151479 ENTQ179TR
9	18	90.0	963	BH155570	BH155570 ENTS128TF
10	17.4	87.0	630	CV007480	CV007480 zfi01-12m
11	17.4	87.0	653	CD306610	CD306610 StrPu691..
12	17.4	87.0	760	BX958633	BX958633 Reverse s
13	17.4	87.0	834	CR243660	CR243660 Reverse s
14	17.4	87.0	1604	AL692767	AL692767 Reverse s
15	17	85.0	278	AA847512	AA847512 oel9c01.s
16	17	85.0	278	AA847520	AA847520 oel9c10.s
17	17	85.0	381	M75738	M75738 CEL01M1S1
18	17	85.0	499	AJ563859	AJ563859 BJ563859
19	17	85.0	504	BJ554532	BJ554532 BJ554532
20	17	85.0	509	AJ562795	AJ562795 BJ562795
21	17	85.0	510	BJ565764	BJ565764 BJ565764
22	17	85.0	562	BJ559871	BJ559871 BJ559871
23	17	85.0	1421	BM556682	BM556682 AGENCOURT
24	17	85.0	1906	CR703050	CR703050 Tetraodon

C 25 16.8 84.0 283 2 BE339708
 26 16.8 84.0 325 5 BP752611
 27 16.8 84.0 350 9 CG397380
 28 16.8 84.0 402 8 AZ195266
 29 16.8 84.0 443 8 AQ184987
 30 16.8 84.0 490 2 BE444732
 31 16.8 84.0 509 2 BE446001
 32 16.8 84.0 513 7 CN856183
 33 16.8 84.0 528 2 BE443711
 34 16.8 84.0 529 2 BE444665
 35 16.8 84.0 529 8 AQ378083
 36 16.8 84.0 529 8 AQ511337
 37 16.8 84.0 555 6 CD452707
 38 16.8 84.0 566 7 CF367946
 39 16.8 84.0 669 6 CA115075
 40 16.8 84.0 677 8 BZ021585
 41 16.8 84.0 677 9 CE675048
 42 16.8 84.0 678 5 BQ514206
 43 16.8 84.0 685 8 BH095996
 44 16.8 84.0 686 7 CK953792
 45 16.8 84.0 689 8 BZ001535

ALIGNMENTS

RESULT 1
AZ541838/c

LOCUS
DEFINITION

ACCSSION
VERSION

KEYWORDS
SOURCE

ORGANISM
REFERENCE

AUTHORS
TITLE

JOURNAL
COMMENT

AZ541838 941 bp DNA linear GSS 14-NOV-2000
 ENTFO93TR Entamoeba histolytica sheared DNA Entamoeba histolytica
 genomic, genomic survey sequence.

AZ541838 GI:11149946
 GSS.

Entamoeba histolytica
 Entamoeba histolytica
 Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 941)
 Loftus, B., Van Aken, S. and Fraser, C.

Determination of clone end sequences from Entamoeba histolytica
 HM1:IMSS sheared DNA library

Unpublished (2000)
 Contact: Brendan J Loftus

Department of Eukaryotic Genomics
 The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0208

Fax: 301 838 3543
 Email: b.loftus@tigr.org

Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
 DNA library

Seq primer: M13-Reverse
 Class: shotgun

High quality sequence start: 15
 High quality sequence stop: 732.

FEATURES
source

1..941
 /organism="Entamoeba histolytica"
 /mol_type="genomic DNA"
 /strain="HM1:IMSS"
 /db_xref="taxon:5759"
 /clone_lib="Entamoeba histolytica sheared DNA"
 /note="Vector: PHOSI; Site 1: Bst I; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from broth cultures of E. histolytica
 using a method described by Clark and Diamond (Clark,
 C.G. and Diamond, L.S. (1993) Entamoeba histolytica: a
 method for isolate identification. Exp. Parasitol.
 77:450.). The DNA was mechanically sheared to give a
 tight size distribution (~2 kb). The v + i method used for
 the library construction is described in detail in Smith,
 H.O. and Venter, J.C. (Making small insert libraries for
 whole genome shotgun sequencing projects. In Genome

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2005, 07:10:45 ; Search time 74.8718 Seconds
(without alignments)
437.088 Million cell updates/sec

Title: US-10-009-980B-5
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	16.8	84.0	601	4	US-09-949-016-36311, A
C 2	16.8	84.0	601	4	US-09-949-016-36312, A
C 3	16.8	84.0	601	4	US-09-949-016-36313, A
C 4	16.8	84.0	601	4	US-09-949-016-86588, A
C 5	16.8	84.0	601	4	US-09-949-016-86589, A
C 6	16.8	84.0	601	4	US-09-949-016-86590, A
C 7	16.8	84.0	601	4	US-09-949-016-163281, A
C 8	16.8	84.0	601	4	US-09-949-016-163282, A
C 9	16.8	84.0	601	4	US-09-949-016-163283, A
C 10	16.8	84.0	601	4	US-10-142-231-49, A
C 11	16.8	84.0	119930	4	US-09-949-016-12677, A
C 12	16.8	84.0	119931	4	US-09-949-016-16319, A
C 13	16.8	84.0	125536	4	US-09-949-016-14186, A
C 14	16.4	82.0	601	4	US-09-949-016-61297, A
C 15	16.4	82.0	601	4	US-09-949-016-61298, A
C 16	16.4	82.0	601	4	US-09-949-016-67735, A
C 17	16.4	82.0	601	4	US-09-949-016-67736, A
C 18	16.4	82.0	601	4	US-09-949-016-67737, A
C 19	16.4	82.0	47199	4	US-09-949-016-12144, A
C 20	16.4	82.0	47200	4	US-09-949-016-13526, A
C 21	16.4	82.0	163181	4	US-09-949-016-13730, A
C 22	16.4	82.0	268449	4	US-09-949-016-17244, A
C 23	16	80.0	17593	4	US-09-949-016-12145, A
C 24	16	80.0	17593	4	US-09-949-016-15734, A
C 25	15.8	79.0	400	4	US-08-956-171B-3796, Ap
C 26	15.8	79.0	400	4	US-08-781-986A-3796, Ap
C 27	15.8	79.0	410	4	US-09-270-767-6237, Ap

ALIGNMENTS

RESULT 1

US-09-949-016-36311/c
; Sequence 36311, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36311
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-36311

Query Match 84.0%; Score 16.8; DB 4; Length 601;
Best Local Similarity 90.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCAAACAGATGGAGTCG 20
|||
Db 41 TCCTAAACAGATGGAGTTG 22

RESULT 2

US-09-949-016-36312/c
; Sequence 36312, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

Sequence 21519, A
Sequence 14592, A
Sequence 945, App
Sequence 24, App
Sequence 193, App
Sequence 191, App
Sequence 15873, A
Sequence 14432, A
Sequence 14433, A
Sequence 12609, A
Sequence 17567, A
Sequence 16246, A
Sequence 22355, A
Sequence 25584, A
Sequence 193956, A
Sequence 6018, Ap
Sequence 12126, A

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2005, 08:35:46 ; Search time 339.487 Seconds
(without alignments)
385.812 Million cell updates/sec

Title: US-10-009-980B-5
Perfect score: 20
Sequence: 1 tccaaacaagatggatcg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 327456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
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- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	20	100.0	20	18	US-10-009-980B-5
2	20	100.0	405	18	US-10-009-980B-9
3	17	85.0	278	9	US-09-867-701-8209
4	16.8	84.0	745	13	US-10-027-632-14575
5	16.8	84.0	745	13	US-10-027-632-14576
6	16.8	84.0	745	13	US-10-027-632-14577
7	16.8	84.0	745	13	US-10-027-632-14578

8	16.8	84.0	745	17	US-10-027-632-14575	Sequence 14575, A
9	16.8	84.0	745	17	US-10-027-632-14576	Sequence 14576, A
10	16.8	84.0	745	17	US-10-027-632-14577	Sequence 14577, A
11	16.8	84.0	745	17	US-10-027-632-14578	Sequence 14578, A
12	16.8	84.0	1452	14	US-10-142-231-49	Sequence 49, Appl
13	16.8	84.0	1452	16	US-10-356-153-49	Sequence 49, Appl
14	16.8	84.0	1452	20	US-10-884-115-49	Sequence 49, Appl
15	16.8	84.0	495269	17	US-10-398-221-2058	Sequence 8, Appl
16	16.8	84.0	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
17	16.4	82.0	25	21	US-10-719-900-612681	Sequence 612681,
18	16.4	82.0	15456	10	US-09-900-112-35	Sequence 35, Appl
19	16.4	82.0	15456	10	US-09-900-112-36	Sequence 35, Appl
20	16.4	82.0	52479	11	US-09-997-722-61	Sequence 61, Appl
21	16.4	82.0	1790242	20	US-10-719-993-6940	Sequence 6940, Ap
22	16	80.0	422	19	US-10-437-963-13717	Sequence 13717, A
23	16	80.0	466	19	US-10-674-124A-16055	Sequence 16055, A
24	16	80.0	608	20	US-10-425-115-34769	Sequence 34769, A
25	16	80.0	670	20	US-10-425-115-143096	Sequence 143096,
26	16	80.0	49088	13	US-10-087-192-13	Sequence 13, Appl
27	16	80.0	56773	19	US-10-331-053-47	Sequence 47, Appl
28	16	80.0	154817	17	US-10-085-117-334	Sequence 334, App
29	15.8	79.0	269	9	US-09-867-701-10410	Sequence 10410, A
30	15.8	79.0	280	17	US-10-374-780A-1371	Sequence 1371, Ap
31	15.8	79.0	280	18	US-10-412-699B-1500	Sequence 1500, Ap
32	15.8	79.0	379	18	US-10-424-599-106566	Sequence 106566,
33	15.8	79.0	400	8	US-08-781-986A-3796	Sequence 3796, Ap
34	15.8	79.0	400	18	US-10-329-624-3796	Sequence 3796, Ap
35	15.8	79.0	401	9	US-09-795-668-610	Sequence 610, App
36	15.8	79.0	401	9	US-09-795-668-610	Sequence 610, App
37	15.8	79.0	401	9	US-09-946-807-610	Sequence 610, App
38	15.8	79.0	457	10	US-09-918-995-34664	Sequence 34664, A
39	15.8	79.0	503	9	US-09-867-701-1827	Sequence 1827, Ap
40	15.8	79.0	553	9	US-09-864-761-8388	Sequence 8388, Ap
41	15.8	79.0	556	20	US-10-425-115-177887	Sequence 177887,
42	15.8	79.0	561	9	US-09-864-761-17463	Sequence 17463, A
43	15.8	79.0	600	22	US-10-972-079-11643	Sequence 11643, A
44	15.8	79.0	684	21	US-10-487-901-2193	Sequence 2193, Ap
45	15.8	79.0	969	9	US-09-864-761-9173	Sequence 9173, Ap

ALIGNMENTS

RESULT 1
US-10-009-980B-5
; Sequence 5, Application US/10009980B
; Publication No. US20040072155A1
; GENERAL INFORMATION:
; APPLICANT: CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
; TITLE OF INVENTION: MOLECULAR METHODS FOR DETECTING GUAR GUM ADDITIONS
; TITLE OF INVENTION: TO LOCUST BEAN GUM
; FILE REFERENCE: PATENT APPLICATION PCT/ES01/00079
; CURRENT APPLICATION NUMBER: US/10/009,980B
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: ES2000000560
; PRIOR FILING DATE: 2000-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence:oligo ITS2
US-10-009-980B-5

Query Match	100.0%;	Score 20;	DB 18;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 5.6;		
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
Qy	1	TCCAAACAAGATGGATCG	20	
Db	1	TCCAAACAAGATGGATCG	20	

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2005, 06:11:10 ; Search time 863.769 Seconds
(without alignments)
1065.851 Million cell updates/sec

Title: US-10-009-980b-6

Perfect score: 19
Sequence: 1 tgcctggcgctgcgcgcgc 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_rts.*
12: gb_ey.*
13: gb_un.*
14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	405	8	CTE245577
2	19	100.0	763	8	AF274687 Cyamopsis
3	17.4	91.6	173	8	AF482510 Utricular
4	17.4	91.6	599	8	AF187091 Pterodon
5	17.4	91.6	602	8	MRU492617 Mitragyna
6	17.4	91.6	613	8	AF086828 Arbutus m
7	17.4	91.6	618	8	AY348776 Impatiens
8	17.4	91.6	620	8	AF467041 Cyclobi
9	17.4	91.6	625	8	AY429098 Oparanthu
10	17.4	91.6	637	8	AF091957 Arbutus x
11	17.4	91.6	639	8	AF091958 Arbutus a
12	17.4	91.6	640	8	AF091956 Arbutus p
13	17.4	91.6	641	8	AF091955 Arbutus o
14	17.4	91.6	642	8	AF061889 Dubautia
15	17.4	91.6	642	8	AF061890 Dubautia
16	17.4	91.6	642	8	AF061891 Dubautia
17	17.4	91.6	642	8	AF061893 Dubautia
18	17.4	91.6	642	8	AF061894 Dubautia
19	17.4	91.6	642	8	AF061896 Dubautia

20	17.4	91.6	642	8	AF061903 Dubautia
21	17.4	91.6	642	8	AF061904 Dubautia
22	17.4	91.6	642	8	AF061905 Dubautia
23	17.4	91.6	642	8	AF061912 Dubautia
24	17.4	91.6	643	8	AF45865 Ichthyoch
25	17.4	91.6	643	8	AY092902 Myosotidi
26	17.4	91.6	644	8	AF331961 Bidens co
27	17.4	91.6	644	8	AF331962 Bidens co
28	17.4	91.6	719	8	AY634977 Polypleis
29	17.4	91.6	300363	1	AE016781 Pseudomon
30	17.4	91.6	302998	1	AE016921 Chromobac
31	17	89.5	608	8	AY209333 Orobanch
32	17	89.5	642	8	AF061899 Dubautia
33	16.4	86.3	318	8	AF412888 Barnadesi
34	16.4	86.3	436	6	I01733 Sequence 3
35	16.4	86.3	528	8	AF315496 Camellia
36	16.4	86.3	585	1	RMN1FKDH2
37	16.4	86.3	607	8	AF531087 Brunnera
38	16.4	86.3	622	8	AF456266 Pyrenaria
39	16.4	86.3	624	8	AF229259 Blepharis
40	16.4	86.3	626	8	AY034853 Hebe macr
41	16.4	86.3	630	8	AF456277 Tutcheria
42	16.4	86.3	630	8	AF456280 Tutcheria
43	16.4	86.3	631	8	AF456281 Tutcheria
44	16.4	86.3	634	8	AF456273 Tutcheria
45	16.4	86.3	642	8	AF456267 Pyrenaria

ALIGNMENTS

RESULT 1	CTE245577	405 bp	DNA	linear	PLN 06-AUG-2002
LOCUS	Cyamopsis tetragonoloba partial 5.8S rRNA gene and ITS 2, isolate				
DEFINITION	seed 10.				
ACCESSION	AJ245577				
VERSION	AJ245577.1	GI:22138754			
KEYWORDS	26S ribosomal RNA; 26S rRNA gene; 5.8S ribosomal RNA; 5.8S rRNA gene; internal transcribed spacer 2; ITS2.				
SOURCE	Cyamopsis tetragonoloba (guar)				
ORGANISM	Cyamopsis tetragonoloba				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Indigoferaceae; Cyamopsis.				
REFERENCE	1				
AUTHORS	Domenech-Sanchez,A., Hernandez,M.L., Rossello,J.A. and Benedi,V.J.				
TITLE	Method for detecting additions of guar gum to locust bean gum				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 405)				
AUTHORS	Domenech-Sanchez,A.				
TITLE	Direct Submission				
JOURNAL	Submitted (05-AUG-1999) Domenech-Sanchez A., Biologia, Area de Microbiologia, Universitat de les illes Balears and IMEDEA (CSIC-UIB), Carretera de Valldemossa, km 7,5; Palma de Mallorca, 07071, SPAIN				
FEATURES	Location/Qualifiers				
source	1..405				
	/organism="Cyamopsis tetragonoloba"				
	/mol_type="genomic DNA"				
	/isolate="seed.10"				
	/db_xref="taxon:3832"				
	/tissue_type="seed"				
gene	1..129				
	/country="India"				
rRNA	/gene="5.8S rRNA"				
	<1..129				
	/gene="5.8S rRNA"				
	/product="5.8S ribosomal RNA"				
misc_feature	130..346				
	/note="internal transcribed spacer 2, ITS2"				
gene	347..405				

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2005, 05:41:19 ; Search time 209.487 Seconds
(without alignments)
536.907 Million cell updates/sec

Title: US-10-009-980B-6
Perfect score: 19
Sequence: 1 tgcctggcgtcgcgctc 19

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1980s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	4	AH44595
2	19	100.0	405	4	AH44598
C 3	16.4	86.3	654	13	ADT42091
C 4	16.4	86.3	1065	13	ADT48263
C 5	16.4	86.3	4216	1	AA70558
C 6	16.4	86.3	110000	2	AAV30458_4
C 7	16.4	86.3	110000	2	AAV30459_4
C 8	16.4	86.3	110000	4	AAI99682_27
C 9	16.4	86.3	110000	4	AAI99683_27
C 10	15.8	83.2	284	8	ABX45083
C 11	15.8	83.2	474	11	ABD14195
C 12	15.8	83.2	708	13	ADS48930
C 13	15.8	83.2	754	6	AAD23833
C 14	15.8	83.2	870	2	AAI18428
C 15	15.8	83.2	870	6	AAD23815
C 16	15.8	83.2	875	2	AAI18432
C 17	15.8	83.2	875	2	AAI18431
C 18	15.8	83.2	875	2	AAI18427
C 19	15.8	83.2	875	6	AAD23814
C 20	15.8	83.2	875	6	AAD23818

C 21	15.8	83.2	875	6	AAD24231	Aad24231 Alternati
C 22	15.8	83.2	875	6	AAD23812	Aad23812 Panax qui
C 23	15.8	83.2	1053	6	AD53368	Ad53368 PEN-1 tel
C 24	15.8	83.2	1053	6	AD53211	Ad53211 PEN-1 tel
C 25	15.8	83.2	1053	9	ADA66135	Ada66135 DNAP-rela
C 26	15.8	83.2	1620	11	ABD14380	Abd14380 Pseudomon
C 27	15.8	83.2	1632	5	AAH77875	Aah77875 Nucleotid
C 28	15.8	83.2	1632	8	ACA51799	Aca51799 Prokaryot
C 29	15.8	83.2	1800	11	ABD13892	Abd13892 Pseudomon
C 30	15.8	83.2	9006	5	AAH77873	Aah77873 Nucleotid
C 31	15.8	83.2	11658	4	ABL17680	Ab117680 Drosophil
C 32	15.4	81.1	121	6	ABK26702	Abk26702 Waxy star
C 33	15.4	81.1	121	6	ABK26694	Abk26694 Waxy star
C 34	15.4	81.1	121	6	ABK26698	Abk26698 Waxy star
C 35	15.4	81.1	121	6	ABK26697	Abk26697 Waxy star
C 36	15.4	81.1	121	6	ABK26701	Abk26701 Waxy star
C 37	15.4	81.1	121	6	ABK26693	Abk26693 Waxy star
C 38	15.4	81.1	121	12	ADN45385	Adn45385 Mutant ce
C 39	15.4	81.1	121	12	ADN45388	Adn45388 Mutant ce
C 40	15.4	81.1	121	12	ADN45384	Adn45384 Mutant ce
C 41	15.4	81.1	121	12	ADN45389	Adn45389 Mutant ce
C 42	15.4	81.1	121	12	ADN45392	Adn45392 Mutant ce
C 43	15.4	81.1	121	12	ADN45393	Adn45393 Mutant ce
C 44	15.4	81.1	537	11	ABD16439	Abd16439 Pseudomon
C 45	15.4	81.1	723	8	ACA50980	Aca50980 Prokaryot

ALIGNMENTS

RESULT 1

AAH44595
ID AAH44595 standard; DNA; 19 BP.

AC AAH44595;

DT 01-NOV-2001 (first entry)

DE Guar and locust bean seed differentiation PCR primer PG22.

KW Guar gum; locust bean gum; detection; plant; initiator; amplification;
KW PCR; Cyanopsis tetragonoloba; Ceratonia siliqua; thickener;
KW Gelling agent; food stabiliser; differentiation; PCR primer; ss.

OS Synthetic.

XX WO200166794-A1.
PD 13-SEP-2001.

XX 02-MAR-2001; 2001WO-ES000079.

XX 08-MAR-2000; 2000ES-00000560.

XX (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
PA (UVIS-) UNIV LAS ISLAS BALEARES.
PA (UVVA-) UNIV VALENCIA.
PA (CARO-) CAROB SA.

PI Benedi Benito VJ, Domenech Sanchez A, Hernandez Viadel ML;
PI Alberti Serrano S, Rossello Picornell JA;
XX WPI; 2001-565598/63.

PT Differentiating between guar and locust bean seeds, or derived gums, by
amplifying specific, characteristic regions of ribosomal DNA.

PS Claim 4; Fig 1; 44pp; Spanish.

XX The present invention describes a method for differentiating between
CC seeds of Cyanopsis tetragonoloba (guar) and Ceratonia siliqua (locust
CC bean) from differences in rDNA extracted from them. The seeds are
germinated, DNA extracted and amplified by polymerase chain reaction

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2005, 06:13:55 ; Search time 1672 Seconds
(without alignments)
432.549 Million cell updates/sec

Title: US-10-009-980b-6

Perfect score: 19
Sequence: 1 tgcctggcgctgcgcgtc 19

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST.*

1: gb_est1.*

2: gb_est2.*

3: gb_hic.*

4: gb_est3.*

5: gb_est4.*

6: gb_est5.*

7: gb_est6.*

8: gb_gss1.*

9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.4	91.6	699	8	CC117786
2	17.4	91.6	712	8	CC129374
3	17.4	91.6	786	9	CC852692
4	17.4	91.6	806	8	CC075421
5	17.4	91.6	840	8	CC080902
6	17.4	91.6	882	8	CC071397
7	17.4	91.6	905	9	CG381256
8	17.4	91.6	917	8	CC101845
9	17.4	91.6	939	9	CG381268
10	17.4	91.6	940	9	CG084378
11	17.4	91.6	998	9	CG084375
12	17.4	89.5	996	2	BE739997
13	16.4	86.3	332	7	CC101845
14	16.4	86.3	357	1	AL831066
15	16.4	86.3	366	2	BE419987
16	16.4	86.3	403	1	AI737701
17	16.4	86.3	432	6	CA012158
18	16.4	86.3	454	6	CD893052
19	16.4	86.3	464	6	CA710712
20	16.4	86.3	477	6	CD923546
21	16.4	86.3	504	6	CA400135
22	16.4	86.3	511	1	AU245885
23	16.4	86.3	522	7	CN864876
24	16.4	86.3	529	6	CB858536

C	25	16.4	86.3	532	4	BJ211978
C	26	16.4	86.3	533	1	AI670298
C	27	16.4	86.3	535	2	BE517064
C	28	16.4	86.3	535	7	CN914909
C	29	16.4	86.3	543	7	CN912613
C	30	16.4	86.3	554	6	CD442907
C	31	16.4	86.3	556	1	AI737987
C	32	16.4	86.3	561	1	AI657458
C	33	16.4	86.3	563	5	EX266910
C	34	16.4	86.3	565	5	BQ467498
C	35	16.4	86.3	567	4	BJ304612
C	36	16.4	86.3	567	7	CN894586
C	37	16.4	86.3	574	5	EX266909
C	38	16.4	86.3	580	7	CN948867
C	39	16.4	86.3	590	7	CV084369
C	40	16.4	86.3	591	5	BQ467224
C	41	16.4	86.3	591	7	CN902278
C	42	16.4	86.3	594	6	CA730170
C	43	16.4	86.3	597	4	BI222007
C	44	16.4	86.3	597	5	BP449990
C	45	16.4	86.3	601	7	CN901560

ALIGNMENTS

RESULT 1
CC117786
LOCUS
DEFINITION
CC117786 699 bp DNA linear GSS 16-APR-2003
NDL.31A3.T7 Notre Dame Liverpool Aedes aegypti genomic clone
NDL.31A3, genomic survey sequence.
CC117786
CC117786.1 GI:29986841
GSS.
SOURCE
Aedes aegypti (yellow fever mosquito)
ORGANISM
Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Aedes;
Stegomyia.
REFERENCE
1 (bases 1 to 699)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
JOURNAL
Other GSSs: NDL.31A3.SP6
CONTACT: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.

FEATURES

source
Location/Qualifiers
1..699
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL.31A3"
/clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

ORIGIN

Query Match 91.6%; Score 17.4; DB 8; Length 699;
Best Local Similarity 94.7%; Pred. No. 8.6e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCCTGGCGCTCGCGGTC 19

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OM nucleic - nucleic search, using sw model

Run on: September 5, 2005, 07:10:45 ; Search time 71.1282 Seconds
(without alignments)
437.088 Million cell updates/sec

Title: US-10-009-980B-6

Perfect score: 19

Sequence: 1 tgcctggcgctgcgcgtc 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	86.3	536165	4	US-09-214-808-1
2	16.4	86.3	4403785	3	US-09-103-840A-2
3	16.4	86.3	4411529	3	US-09-103-840A-1
4	16	84.2	582	4	US-09-902-540-3481
5	16	84.2	17188	4	US-09-902-540-1166
6	15.8	83.2	474	4	US-09-252-991A-12799
7	15.8	83.2	754	3	US-09-541-941B-26
8	15.8	83.2	870	2	US-08-778-912A-4
9	15.8	83.2	870	3	US-09-541-941B-4
10	15.8	83.2	875	2	US-08-778-912A-2
11	15.8	83.2	875	2	US-08-778-912A-3
12	15.8	83.2	875	2	US-08-778-912A-7
13	15.8	83.2	875	3	US-09-541-941B-1
14	15.8	83.2	875	3	US-09-541-941B-3
15	15.8	83.2	875	3	US-09-541-941B-7
16	15.8	83.2	1053	4	US-09-940-244-393
17	15.8	83.2	1620	4	US-09-252-991A-12984
18	15.8	83.2	1800	4	US-09-252-991A-12986
19	15.8	83.2	4455	4	US-09-902-540-7119
20	15.8	83.2	4458	4	US-09-902-540-650
21	15.4	81.1	350	3	US-08-651-155B-36
22	15.4	81.1	350	4	US-09-194-036B-36
23	15.4	81.1	537	4	US-09-252-991A-15043
24	15.4	81.1	1014	4	US-09-252-991A-15043
25	15.4	81.1	1017	4	US-09-252-991A-15183
26	15.4	81.1	1239	4	US-09-902-540-7944
27	15.4	81.1	1242	4	US-09-902-540-4840

c	28	15.4	81.1	1437	4	US-09-252-991A-1434	Sequence 1434, Ap
	29	15.4	81.1	1473	4	US-09-252-991A-1584	Sequence 1584, Ap
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c	34	15.4	81.1	21758	4	US-09-902-540-1238	Sequence 1238, Ap
	35	15.4	81.1	39949	4	US-09-949-016-14210	Sequence 14210, A
	36	15	78.9	405	4	US-09-252-991A-4225	Sequence 4225, Ap
c	37	15	78.9	843	4	US-09-252-991A-4551	Sequence 4551, Ap
c	38	15	78.9	1128	4	US-09-252-991A-4450	Sequence 4450, Ap
	39	15	78.9	1242	4	US-09-252-991A-4304	Sequence 4304, Ap
	40	15	78.9	1302	4	US-09-252-991A-4157	Sequence 4157, Ap
c	41	15	78.9	3333	4	US-09-902-540-4753	Sequence 4753, Ap
	42	15	78.9	14809	4	US-09-902-540-1032	Sequence 1032, Ap
	43	15	78.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	44	15	78.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	45	14.8	77.9	390	4	US-09-902-540-7078	Sequence 7078, Ap

ALIGNMENTS

RESULT 1

US-09-214-808-1

; Sequence 1, Application US/09214808A

; Patent No. 6475793

; GENERAL INFORMATION:

; APPLICANT: Rosenthal, Andre

; APPLICANT: Freiberg, Christoph

; APPLICANT: Perret, Xavier Philippe

; APPLICANT: Broughton, William John

; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic

; Patent No. 6475793

; TITLE OF INVENTION: Plasmid

; FILE REFERENCE: CARP0068

; CURRENT APPLICATION NUMBER: US/09/214.808A

; PRIOR FILING DATE: 1999-06-22

; PRIOR APPLICATION NUMBER: PCT/IB97/00950

; PRIOR FILING DATE: 1997-07-10

; NUMBER OF SEQ ID NOS: 1

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 536165

; TYPE: DNA

; ORGANISM: Rhizobium

US-09-214-808-1

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Best Local Similarity 94.4%; Pred. No. 1.3e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 453718 GCCTGGCGTCGCGCATC 453735

RESULT 2

US-09-103-840A-2/c

; Sequence 2, Application US/09103840A

; Patent No. 6294328

; GENERAL INFORMATION:

; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.

; APPLICANT: FRASER, Claire M.

; APPLICANT: VENTER, John C.

; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

; FILE REFERENCE: 24366-20007.00

; CURRENT APPLICATION NUMBER: US/09/103,840A

; CURRENT FILING DATE: 1998-06-24

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

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Run on: September 5, 2005, 08:35:46 ; Search time 322.513 Seconds
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Title: US-10-009-980B-6

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	16.4	86.3	624	20	US-10-425-115-39345

C	8	16.4	86.3	654	17	US-10-369-493-40529	Sequence 40529, A
C	9	16.4	86.3	738	20	US-10-425-115-39179	Sequence 39179, A
C	10	16.4	86.3	925	20	US-10-425-115-174017	Sequence 174017, A
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C	13	16.4	86.3	1527	20	US-10-425-115-18205	Sequence 18205, A
C	14	16.4	86.3	2649	19	US-10-437-963-112	Sequence 112, App
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C	19	15.8	83.2	284	9	US-09-960-352-10248	Sequence 10248, A
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C	24	15.8	83.2	708	17	US-10-369-493-27360	Sequence 27360, A
C	25	15.8	83.2	754	9	US-09-897-231-26	Sequence 26, Appli
C	26	15.8	83.2	759	20	US-10-425-115-53318	Sequence 53318, A
C	27	15.8	83.2	807	20	US-10-425-115-137985	Sequence 137985, A
C	28	15.8	83.2	855	20	US-10-425-115-45730	Sequence 45730, A
C	29	15.8	83.2	859	20	US-10-425-115-70138	Sequence 70138, A
C	30	15.8	83.2	870	9	US-09-897-231-4	Sequence 4, Appli
C	31	15.8	83.2	875	9	US-09-897-231-1	Sequence 1, Appli
C	32	15.8	83.2	875	9	US-09-897-231-3	Sequence 3, Appli
C	33	15.8	83.2	875	9	US-09-897-231-7	Sequence 7, Appli
C	34	15.8	83.2	938	20	US-10-425-115-70438	Sequence 70438, A
C	35	15.8	83.2	972	20	US-10-425-115-166184	Sequence 166184, A
C	36	15.8	83.2	996	20	US-10-425-115-56079	Sequence 56079, A
C	37	15.8	83.2	1023	20	US-10-425-115-142243	Sequence 142243, A
C	38	15.8	83.2	1053	10	US-09-940-244-393	Sequence 393, App
C	39	15.8	83.2	1053	12	US-09-732-622A-393	Sequence 393, App
C	40	15.8	83.2	1053	20	US-10-309-584-393	Sequence 393, App
C	41	15.8	83.2	1053	21	US-10-783-557-394	Sequence 394, App
C	42	15.8	83.2	1233	20	US-10-425-115-143856	Sequence 143856, A
C	43	15.8	83.2	1291	20	US-10-425-115-57660	Sequence 57660, A
C	44	15.8	83.2	1553	20	US-10-425-115-118641	Sequence 118641, A
C	45	15.8	83.2	1632	17	US-10-382-122A-39669	Sequence 39669, A

ALIGNMENTS

RESULT 1
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; Sequence 6, Application US/10009980B
; Publication No. US20040072155A1
; GENERAL INFORMATION:
; APPLICANT: CONSEJO SUPERIOR DE INVESTIGACIONES CIENTIFICAS
; TITLE OF INVENTION: MOLECULAR METHODS FOR DETECTING GUAR GUM ADDITIONS
; FILE REFERENCE: PATENT APPLICATION PCT/ES01/00079
; CURRENT APPLICATION NUMBER: US/10/009,980B
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: ES2000000560
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the Artificial Sequence:oligo PG22
US-10-009-980B-6

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Best Local Similarity	100.0%	Pred. No. 17;	Mismatches 0;	Indels 0;
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